IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Baker et al.	Docket No:	39780-2830P1C47
Serial No:	10/015,671	Group Art Unit:	1647
Filed:	December 11, 2001	Examiner:	Rachel K. Hunnicutt

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF NAPOLEONE FERRARA, Ph.D., AUDREY GODDARD, Ph.D., PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D., JAMES PAN, Ph.D., COLIN K. WATANABE and WILLIAM I. WOOD, Ph.D. UNDER 37 CFR 1.131

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2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by U.S. Patent Publication No. 2003/0096951 (Jacobs *et al.*, publication date May 22, 2003 and effective filing date August 14, 1998).

3. The polypeptide designated as PRO1244 (SEQ ID NO:130) claimed in the above-identified application in the United States was sequenced and cloned prior to August 14, 1998.

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James Pan, Ph.D.	Date
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10. The DNA-64883 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 129 disclosed in the above-identified application.

11. The beginning of the cDNA sequence corresponding to SEQ ID NO: 129 in the above-identified application is shown on page 1 of the GSeqEdit database report, and the location of the first nucleotide is marked with "^insert starts here" and an arrow. The location of the last nucleotide corresponding to SEQ ID NO: 129 is shown on page 11 and is marked with an arrow.

12. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 130 disclosed in the above-identified application.

13. The first 26 amino acid residues of the PRO1244 polypeptide (SEQ ID NO:130) encoded by the cDNA (DNA-64883) are also shown on page 1 of the GSeqEdit report and the remaining 309 residues appear on pages 2-6 of the report.

14. All activities listed under paragraphs 4-13 were completed prior to August 14, 1998. (See Exhibit A).

15. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Napoleone Ferrara, Ph.D.	Date
Audrey Goddard, Ph.D.	Date
Paul J. Godowski, Ph.D.	Date
James Pan, Ph.D.	Date
Austin Gurney, Ph.D.	Date
Colin K. Watanabe	Date
William I. Wood, Ph.D.	10/5/04 Date

>[redacted]

>DNA64883 [Full]

>510 Sites [All Sites]

>[redacted] DNA64883 wiw GSeqEdit

>[redacted] DNA64883 zemin GSeqEdit

>[redacted] DNA64883 goddarda GSeqEdit

>[redacted] DNA64883 sheldens GSeqEdit

>HBN64883.seq, sequenced at ABI/ACGT by Peter Ma and Ellson Chen

>human ortholog of implantation-associated protein - Rattus

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                                                                nlaIII
              mnlI                                              mslI
            taqI                                               styI
           xhoI                thaI                            ncoI
           tliI                fnuDII/mvnI                     dsaI          tseI
           smlI               hinPI   aciI                     btgI/bstDSI   fnu4HI/bsoFI
           paeR7I  mwoI     tseI bstUI[M.hhaI-]                bstXI         bbvI                  dde
      tsp509I[M.ecoRI-]     fnu4HI/bsoFI                       bsaJI       hinPI            taiI   bsp
     ecoRI     avaI[M.taqI-]  bbvI bsh1236I                tsp45I          hhaI/cfoI        maeII/hpyC
     apoI   mwoI bseRI   nlaIII  hhaI/cfoI           bsmAI maeIII         haeII        hpy99I   mnlI
  1 CGGAATTCGG CTCGAGGAGC GAACATGGCA GCGCGTTGGC GGTTTTGGTG TGTCTCTGTG ACCATGGTGG TGGCGCTGCT CATCGTTTGC GACGTTCCCT
    GCCTTAAGCC GAGCTCCTCG CTTGTACCGT CGCGCAACCG CCAAAACCAC ACAGAGACAC TGGTACCACC ACCGCGACGA GTAGCAAACG CTGCAAGGGA
  1                 ↑        M  A  A  R  W  R  F  W  C  V  S  V  T  M  V  V  A  L  L  I  V  C  D  V  P  S
                    ^insert starts here
                             ^MET
```

```
      mnlI                                                     aluI
     alwNI[dcm-]                                              pvuII
     alw26I/bsmAI           bsaXI        hpy188I              mspAlI/nspBII                                                    bsmAI
 101 CAGCCTCTGC CCAAAGAAAG AAGGAGATGG TGTTATCTGA AAAGGTTAGT CAGCTGATGG AATGGACTAA CAAAAGACCT GTAATAAGAA TGAATGGAGA
     GTCGGAGACG GGTTTCTTTC TTCCTCTACC ACAATAGACT TTTCCAATCA GTCGACTACC TTACCTGATT GTTTTCTGGA CATTATTCTT ACTTACCTCT
  27  A  S  A   Q  R  K   K  E  M  V   L  S  E   K  V  S   Q  L  M  E   W  T  N   K  R  P   V  I  R  M   N  G  D

                                                                   tspRI                  bst4CI/hpyCH4III     cac8I
                                                                   btsI                  ahdI/eam1105I     cac8I
          hpy99I                         tsp509I             nlaIII                 hpyCH4V tspRI          hpyCH4V al
 201 CAAGTTCCGT CGCCTTGTGA AAGCCCCACC GAGAAATTAC TCCGTTATCG TCATGTTCAC TGCTCTCCAA CTGCATAGAC AGTGTGTCGT TTGCAAGCAA
     GTTCAAGGCA GCGGAACACT TTCGGGGTGG CTCTTTAATG AGGCAATAGC AGTACAAGTG ACGAGAGGTT GACGTATCTG TCACACAGCA AACGTTCGTT
  60  K  F  R   R  L  V  K   A  P  P   R  N  Y   S  V  I  V   M  F  T   A  L  Q   L  H  R  Q   C  V  V   C  K  Q
```

```
                                    scrFI[dcm-]
                                    pspGI
                                    mvaI
                                    ecoRII[dcm-]
                                    dsaV[dcm-]
                                    bstNI
                                    bssKI[dcm-]
                                    apyI[dcm+]
                                  sau3AI
                                  mboI/ndeII[dam-]
                                  dpnII[dam-]
                                  dpnI[dam+]
                                  alwI[dam-]       scrFI[dcm-]
                                 bstYI/xhoII       pspGI
                                alwNI[dcm-]        mvaI                                    nlaIII
                                alw26I/bsmAI       ecoRII[dcm-]                           styI
                             tsp509I[M.ecoRI-]     dsaV[dcm-]       hpyCH4V               ncoI
                          ecoRI pflMI[dcm-]        bstNI baeI    tspRI                    dsaI
                          apoI  bslI[dcm-]         bssKI[dcm-]  bsrI bsmI hphI            btgI/bstDSI
                       mboII   hpy188III           apyI[dcm+] bpmI/gsuI[dcm-]             bsaJI                    hpy18
301 GCTGATGAAG AATTCCAGAT CCTGGCAAAC TCCTGGCGAT ACTCCAGTGC ATTCACCAAC AGGATATTTT TTGCCATGGT GGATTTTGAT GAAGGCTCTG
    CGACTACTTC TTAAGGTCTA GGACCGTTTG AGGACCGCTA TGAGGTCACG TAAGTGGTTG TCCTATAAAA AACGGTACCA CCTAAAACTA CTTCCGAGAC
 93 A  D  E  E  F  Q  I  L  A  N  S  W  R  Y  S  S  A  F  T  N  R  I  F  F  A  M  V  D  F  D  E  G  S  D
```

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                        tsp509I[M.ecoRI-]
                       ecoRI                              hpyCH4V
                 sfaNI apoI                              ecoNI
           hpy188I    nlaIII    aluI                     bslI        bslI      hphI    ndeI    maeIII    aciI
401 ATGTATTTCA GATGCTAAAC ATGAATTCAG CTCCAACTTT CATCAACTTT CCTGCAAAAG GGAAACCCAA ACGGGGTGAT ACATATGAGT TACAGGTGCG
    TACATAAAGT CTACGATTTG TACTTAAGTC GAGGTTGAAA GTAGTTGAAA GGACGTTTTC CCTTTGGGTT TGCCCCACTA TGTATACTCA ATGTCCACGC
127  V  F  Q   M  L  N   M  N  S  A   P  T  F   I  N  F   P  A  K  G   K  P  K   R  G  D   T  Y  E  L   Q  V  R

                 ddeI[M.aluI-]
                 bspCNI        mspI    sau3AI
                celII/espI     hpaII   mboI/ndeII[dam-]
                blpI/bpu1102I scrFI[M.hpaII-]                                                  bsmFI
              aluI            nciI    dpnII[dam-]                                              sau96I
             pvuII            dsaV    dpnI[dam+]                                               nlaIV
             mspA1I/nspBII    bssKI alwI[dam-]              sspI                      tsp509I  avaII bslI
501 GGGTTTTTCA GCTGAGCAGA TTGCCCGGTG GATCGCCGAC AGAACTGATG TCAATATTAG AGTGATTAGA CCCCCAAATT ATGCTGGTCC CCTTATGTTG
    CCCAAAAAGT CGACTCGTCT AACGGGCCAC CTAGCGGCTG TCTTGACTAC AGTTATAATC TCACTAATCT GGGGGTTTAA TACGACCAGG GGAATACAAC
160  G  F  S   A  E  Q  I   A  R  W   I  A  D   R  T  D  V   N  I  R   V  I  R   P  P  N  Y   A  G  P   L  M  L

                                    taqI                                                         aluI
                                   sfuI                                                         tseI
                                   bstBI                                      fokI              fnu4HI/bsoFI
                                   bsiCI                  tsp509I   tru9I     bstF5I            bbvI
                            baeI  mboII mboII              apoI     mseI    bsrI      mwoI hpyCH4V
601 GGATTGCTTT TGGCTGTTAT TGGTGGACTT GTGTATCTTC GAAGAAGTAA TATGGAATTT CTCTTTAATA AAACTGGATG GGCTTTTGCA GCTTTGTGTT
    CCTAACGAAA ACCGACAATA ACCACCTGAA CACATAGAAG CTTCTTCATT ATACCTTAAA GAGAAATTAT TTTGACCTAC CCGAAAACGT CGAAACACAA
193 G  L  L  L   A  V  I   G  G  L   V  Y  L  R   R  S  N   M  E  F   L  F  N  K   T  G  W   A  F  A   A  L  C  F
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```
                                                                                       nlaIII          nlaIII
                                                                                      pciI            styI
                                                                                      nspHI           ncoI
                                                 sau96I                    bslI       nspI            dsaI
                                                 avaII                  tfiI          aflIII          btgI/bs
      cac8I      ahdI/eam1105I      nlaIV      mnlI        ndeI         hinfI      bsmFI       tsp509I bsaJI
701 TTGTGCTTGC TATGACATCT GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA CATGTGAATT ATATCCATGG
    AACACGAACG ATACTGTAGA CCAGTTTACA CCTTGGTATA TTCTCCTGGT GGTATACGGG TATTCTTAGG GGTGTGCCCT GTACACTTAA TATAGGTACC
227  V  L  A  M  T  S  G  Q  M  W  N  H  I  R  G  P  P  Y  A  H  K  N  P  H  T  G  H  V  N  Y  I  H  G

                                                                      ddeI                          tseI
                                                                     eco81I                         fnu4HI/bsoFI
                                                    tru9I            bsu36I/mstII/sauI              bbvI      hpy1
           bsrI       aluI                mboII    mseI        maeIII                              aluI      mnlI
801 AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATTGTT CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT
    TTCGTCAGTT CGGGTCAAAC ATCGACTTTG TGTGTAACAA GAAGACAAAT TACCACCTCA ATGGAATCCT TACCACGAAA ATACACTTCG ACGATGGAGA
260 S  S  Q  A  Q  F  V  A  E  T  H  I  V  L  L  F  N  G  G  V  T  L  G  M  V  L  L  C  E  A  A  T  S

                                                                                                    sau3AI
                                                                                                    mboI/ndeII[dam
                                                                                                    dpnII[dam-]
                                                                                  sfaNI             dpnI[dam+]
                                                                        eco57I   fokI              bstYI/xhoII
      nlaIII                                                            mboII    bstF5I            bglII          nl
901 GACATGGATA TTGGAAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTTGTATTA TTCTTCAGTT GGATGCTCTC TATTTTTAGA TCTAAATATC
    CTGTACCTAT AACCTTTCGC TTTCTATTAC ACACACCGAC CATAACCTGA ACAACATAAT AAGAAGTCAA CCTACGAGAG ATAAAAATCT AGATTTATAG
293 D  M  D  I  G  K  R  K  I  M  C  V  A  G  I  G  L  V  V  L  F  F  S  W  M  L  S  I  F  R  S  K  Y  H
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```
                                          bsmFI
                                          sau96I                          bsrI
                                          nlaIV                         rsaI
                                          avaII                       bpmI/gsuI[dcm-]
                                    tru9I  ppuMI                      bsrI   csp6I
                      aluI hpy188I  mseI   eco0109I/draII            tspRI  scaI     tsp509I
1001 ATGGCTACCC ATACAGCTTT CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC GAAAATCGTG TGTGTTTGAA
     TACCGATGGG TATGTCGAAA GACTACTCAA TTTTTCCAGG GTCTCTATAT ATCTGTGACC TCATGACCTT TAACTTTTTG CTTTTAGCAC ACACAAACTT
327   G  Y  P  Y  S  F  L  M  S  O

                                                       tru9I
                                                       mseI    tru9I
       bsmI                                          ahaIII/draI     tru9I                          tru9I
     mboII hpyCH4V                  mnlI             swaI      mseI   mseI       mboII              mseI
1101 AAGAAGAATG CAACTTGTAT ATTTTGTATT ACCTCTTTTT TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC
     TTCTTCTTAC GTTGAACATA TAAAACATAA TGGAGAAAAA AAGTTCACTA AATTTATCAA TTAGTAAATT GGTTTCTTCT ACACATCACG GAATTGTTCG

                 mnlI
                ddeI                                    bsrI                      tsp509I      tru9I
                bspCNI                mnlI tru9I      mboII tspRI               tru9I    rsaI tsp509I
      mnlI     hpy188I            tsp509I   mseI      earI/ksp632I              mseI     csp6I  mseI
1201 AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCTTAACCT TCTCTTCCCA GTGAACTTTA TGGAACATTT AATTTAGTAC AATTAAGTAT
     TTAGGAGACA GTTTTAGACT CCATAAACTT TTATTAATAG GAGAATTGGA AGAGAAGGGT CACTTGAAAT ACCTTGTAAA TTAAATCATG TTAATTCATA

                                                                tru9I
                                                                mseI
                                                               hpaI
      psiI  tsp509I                          aluI              hincII/hindII hpy188I                bslI
1301 ATTATAAAAA TTGTAAAACT ACTACTTTGT TTTAGTTAGA ACAAAGCTCA AAACTACTTT AGTTAACTTG GTCATCTGAT TTTATATTGC CTTATCCAAA
     TAATATTTTT AACATTTTGA TGATGAAACA AAATCAATCT TGTTTCGAGT TTTGATGAAA TCAATTGAAC CAGTAGACTA AAATATAACG GAATAGGTTT
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                    scrFI[dcm-]
                    pspGI
                    mvaI
                    ecoRII[dcm-]
                    dsaV[dcm-]
                    bstNI                                       tsp509I[M.ecoRI-]
                    bssKI[dcm-]                                xmnI
                    apyI[dcm+]                                 ecoRI          mboII
                   sexAI                                       asp700     aluI     mslI       fokI
               hpy188III         ndeI      maeIII              apoI     ddeI[M.aluI-]         bstF5I
1401 GATGGGGAAA GTAAGTCCTG ACCAGGTGTT CCCACATATG CCTGTTACAG ATAACTACAT TAGGAATTCA TTCTTAGCTT CTTCATCTTT GTGTGGATGT
     CTACCCCTTT CATTCAGGAC TGGTCCACAA GGGTGTATAC GGACAATGTC TATTGATGTA ATCCTTAAGT AAGAATCGAA GAAGTAGAAA CACACCTACA

                                                                                                       taiI
                                                                                                  hgiAI/aspHI
                                                                                                  bsp1286
                                                                  hpy188I                         bsiHKAI    rmaI  ddeI
     bstZ17I                                                    mboII                          hpy188I  maeII/hpyCH4IV
     bst1107I                                                  bpuAI                         eco57I   aflIII maeI  bspC
     accI        sfaNI                     tsp509I      nlaIII bbsI                        mboII  bmyI btrI  bfaI mnlI
1501 GTATACTTTA CGCATCTTTC CTTTTGAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC
     CATATGAAAT GCGTAGAAAG GAAAACTCAT CTCTTTAATA CACACAGTAC ACCAGAAGAC TTTTACCTTG TGGTAAGAAG TCTCGTGTGC AGATCGGGAG
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                                                                                tth111I/aspI
                                                                                pleI
                      bseRI                                                     pflFI
                     mnlI                           bpmI/gsuI[dcm-]             mlyI
                    bseRI                       hinPI        ddeI               hinfI
        bst4CI/hpyCH4III mnlI  hpyCH4V          hhaI/cfoI    bspCNI           bsmAI     bsmAI
1601 AGCAAGACAG TTGTTTCTCC TCCTCCTTGC ATATTTCCTA CTGCGCTCCA GCCTGAGTGA TAGAGTGAGA CTCTGTCTCA AAAAAAAGTA TCTCTAAATA
     TCGTTCTGTC AACAAAGAGG AGGAGGAACG TATAAAGGAT GACGCGAGGT CGGACTCACT ATCTCACTCT GAGACAGAGT TTTTTTTCAT AGAGATTTAT

                               tru9I                                                                  tsp45I
                               mseI                         tfiI                                     hphI
          tsp509I            hpaI                xmnI       hinfI                                 tru9I maeIII
      psiI          smlI     hincII/hindII       asp700   hpy188I              ddeI               mseI bstEII
1701 CAGGATTATA ATTTCTGCTT GAGTATGGTG TTAACTACCT TGTATTTAGA AAGATTTCAG ATTCATTCCA TCTCCTTAGT TTTCTTTTAA GGTGACCCAT
     GTCCTAATAT TAAAGACGAA CTCATACCAC AATTGATGGA ACATAAATCT TTCTAAAGTC TAAGTAAGGT AGAGGAATCA AAAGAAAATT CCACTGGGTA

                                                                                                          dde
                  ddeI[M.aluI-]      maeIII        haeIII/palI                     tsp45I               rsaI
                aluI               tspRI         nlaIII                  tsp509I   maeIII               csp6I
1801 CTGTGATAAA AATATAGCTT AGTGCTAAAA TCAGTGTAAC TTATACATGG CCTAAAATGT TTCTACAAAT TAGAGTTTGT CACTTATTCC ATTTGTACCT
     GACACTATTT TTATATCGAA TCACGATTTT AGTCACATTG AATATGTACC GGATTTTACA AAGATGTTTA ATCTCAAACA GTGAATAAGG TAAACATGGA
```

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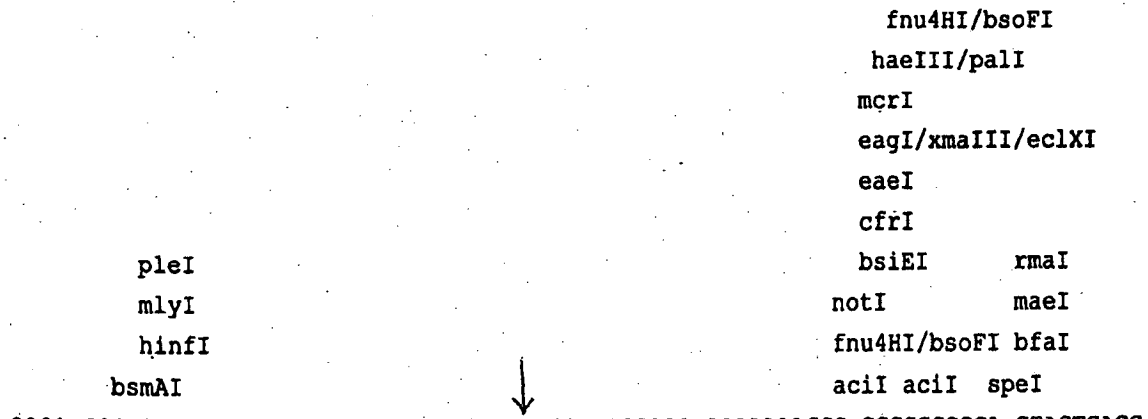
                                            scrFI[dcm-]
                                            pspGI
                                            mvaI
                                            ecoRII[dcm-]
                                            dsaV[dcm-]
                                            bstNI
                                          haeIII/palI
                                         mscI/balI[dcm-]
                                         eaeI[dcm-]
                                         cfrI
                                       scrFI[dcm-]
                                       pspGI
                                       mvaI bssKI[dcm-]
                                       ecoRII[dcm-]   tsp45I
                                       dsaV[dcm-]     maeIII                                                          bssS
                                       bstNI     hinPI                                                               hpy18
                                       bssKI[dcm-]  tspRI                                                           sau3AI
                                 pleI bslI[dcm-] hhaI/cfoI                                          styI cac8I     mboI/nd
                 ddeI            mlyI bsaJI apyI[dcm+]                          ddeI              haeIII/palI     dpnII[d
                 bspCNI          hinfI apyI[dcm+]  btsI                         bspCNI        mnlI bsaJI          dpnI[da
1901 AAGAGAAAAA TAGGCTCAGT TAGAAAAGGA CTCCCTGGCC AGGCGCAGTG ACTTACGCCT GTAATCTCAG CACTTTGGGA GGCCAAGGCA GGCAGATCAC
     TTCTCTTTTT ATCCGAGTCA ATCTTTTCCT GAGGGACCGG TCCGCGTCAC TGAATGCGGA CATTAGAGTC GTGAAACCCT CCGGTTCCGT CCGTCTAGTG
```

```
                                  mscI/ball[dcm-]
                                  eaeI[dcm-]
                                 scrFI[dcm-]
                                 pspGI
                                 mvaI
                                 ecoRII[dcm-]
                                 dsaV[dcm-]
                                 bstNI
                        bsmAI    bssKI[dcm-]
                      taqI   fokI  cfrI    nlaIII         bsmAI
          hpy188III  bsaI bstF5I haeIII/palI           esp3I                    aluI
    mnlI          hpy188III  apyI[dcm+]   hphI       bsmBI                tsp509I                nlaIV
2001 GAGGTCAGGA GTTCGAGACC ATCCTGGCCA ACATGGTGAA ACCCCGTCTC TACTAAAAAT ATAAAAATTA GCTGGGTGTG GTGGCAGGAG CCTGTAATCC
     CTCCAGTCCT CAAGCTCTGG TAGGACCGGT TGTACCACTT TGGGGCAGAG ATGATTTTTA TATTTTTAAT CGACCCACAC CACCGTCCTC GGACATTAGG

                                                                                                    scrFI[dcm-]
                                                                                                    pspGI
                                                                                                    mvaI
                                                                                                    ecoRII[dcm-]
                                                                                        tspRI       dsaV[dcm-]
                                                                                  sau3AI   btsI     bstNI
                        ddeI        tfiI          hpy188III                       mboI/ndeII[dam-]  bssKI[dcm-]
                        bspCNI      hinfI         ddeI                            dpnII[dam-] hpyCH4V  apyI[dcm+]
     aluI       mnlI  mnlI bssSI                 bspCNI      mnlI    tspRI       dpnI[dam+] bsgI  bpmI/gsuI[dcm-]
2101 CAGCTACACA GGAGGCTGAG GCACGAGAAT CACTTGAACT CAGGAGATGG AGGTTTCAGT GAGCCGAGAT CACGCCACTG CACTCCAGCC TGGCAACAGA
     GTCGATGTGT CCTCCGACTC CGTGCTCTTA GTGAACTTGA GTCCTCTACC TCCAAAGTCA CTCGGCTCTA GTGCGGTGAC GTGAGGTCGG ACCGTTGTCT
```



> length: 2269

accI(GTMKAC):	1501
aciI(CCGC):	39 498 2250 2254
aflIII(ACRYGT):	780 1586
ahaIII(TTTAAA):	1150
ahdI(GACNNNNNGTC):	278 714
aluI(AGCT):	152 300 429 510 690 822 888 1015 1345 1476 1816 2070 2102
alw26I(CAGNNNCTG):	101 316
alwI(GGATCNNNN):	318 530
alwNI(CAGNNNCTG):	101 316
apoI(RAATTY):	3 310 423 655 1464
apyI(CCWGG):	321 332 1422 1934 1939 2023 2189
asp700(GAANNNNTTC):	1464 1749
aspHI(GWGCWC):	1582